

L Number	Hits	Search Text	DB	Time stamp
1	611	(alzheimer same disease) and (cholinesterase same inhibitor)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 11:21
3	0	(alzheimer same disease) same (cholinesterase same inhibitor) same treat?	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 11:22
2	271	(alzheimer same disease) same (cholinesterase same inhibitor)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 11:22
4	4	(alzheimer same disease) same (cholinesterase same inhibitor).clm.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 11:22
-	2	daly-james.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 11:21
-	2	kotwal-girish.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 10:22
-	46	vaccinia same complement same control same protein	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 10:24
-	4	(vaccinia same complement same control same protein) and alzheimer	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 10:27
-	4	(vaccinia same complement same control same protein) and alzheime?	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/04/22 10:27

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NEWS 3 JAN 27 Source of Registration (SR) information in REGISTRY updated  
and searchable  
NEWS 4 JAN 27 A new search aid, the Company Name Thesaurus, available in  
CA/CAPLUS  
NEWS 5 FEB 05 German (DE) application and patent publication number format  
changes  
NEWS 6 MAR 03 MEDLINE and L MEDLINE reloaded  
NEWS 7 MAR 03 MEDLINE file segment of TOXCENTER reloaded  
NEWS 8 MAR 03 FRANCEPAT now available on STN  
NEWS 9 MAR 29 Pharmaceutical Substances (PS) now available on STN  
NEWS 10 MAR 29 WPIFV now available on STN  
NEWS 11 MAR 29 No connect hour charges in WPIFV until May 1, 2004  
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NEWS EXPRESS MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT  
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),  
AND CURRENT DISCOVER FILE IS DATED 13 APRIL 2004  
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=> s daly james/au  
L1 17 DALY JAMES/AU

=> s kotwal girish/au  
L2 0 KOTWAL GIRISH/AU

=> s (vaccinia (s) complement (s) control (s) protein) (p) alzheimer  
L3 15 (VACCINIA (S) COMPLEMENT (S) CONTROL (S) PROTEIN) (P) ALZHEIMER

=> dup rem l3  
PROCESSING COMPLETED FOR L3  
L4 6 DUP REM L3 (9 DUPLICATES REMOVED)

=> d l4 total ibib kwic

L4 ANSWER 1 OF 6 MEDLINE on STN DUPLICATE 1  
ACCESSION NUMBER: 2004003750 IN-PROCESS  
DOCUMENT NUMBER: PubMed ID: 14698003  
TITLE: Prolonged retention of vaccinia virus complement control protein following IP injection: implications in blocking xenorejection.  
AUTHOR: Jha P; Smith S A; Justus D E; Kotwal G J  
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Louisville School of Medicine, Louisville, KY 40202, USA.  
SOURCE: Transplantation proceedings, (2003 Dec) 35 (8) 3160-2.  
Journal code: 0243532. ISSN: 0041-1345.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals  
ENTRY DATE: Entered STN: 20040106  
Last Updated on STN: 20040129

AB The **vaccinia virus complement control protein (VCP)** blocks classic and alternate **complement** pathways by binding to the third and fourth **complement** components and by blocking the formation of the C3-convertase as well as by accelerating the decay of the C3 and C4 convertase. The therapeutic potential of VCP has been extensively studied for brain injury, xenotransplantation, **Alzheimer's** disease, and spinal cord injury. We investigated the pharmacokinetic behavior of rVCP in mice. Dosage of rVCP was studied by. . .

L4 ANSWER 2 OF 6 MEDLINE on STN DUPLICATE 2  
ACCESSION NUMBER: 2003213362 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12734405  
TITLE: Vaccinia complement control protein: multi-functional protein and a potential wonder drug.  
AUTHOR: Jha Purushottam; Kotwal Girish J  
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Louisville, School of Medicine, Louisville, KY 40202, USA.  
SOURCE: Journal of biosciences, (2003 Apr) 28 (3) 265-71. Ref: 36  
Journal code: 8100809. ISSN: 0250-5991.  
PUB. COUNTRY: India  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)

LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200403  
ENTRY DATE: Entered STN: 20030508  
Last Updated on STN: 20040324  
Entered Medline: 20040323

AB **Vaccinia virus complement control protein** (VCP) was one of the first viral molecules demonstrated to have a role in blocking **complement** and hence in the evasion of host defense. Structurally it is very similar to the human C4b-BP and the other. . . can take place simultaneously and contribute to its many function and to its potential use in several inflammatory diseases, e.g. **Alzheimer's** disease (AD), CNS injury, xenotransplantation, etc. making it a truly fascinating molecule and potential drug.

L4 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
ACCESSION NUMBER: 2003:145171 BIOSIS  
DOCUMENT NUMBER: PREV200300145171  
TITLE: Potential intervention by **vaccinia virus complement control protein** of the signals contributing to the progression of central nervous system injury to **Alzheimer's** disease.  
AUTHOR(S): Kotwal, Girish J. [Reprint Author]; Lahiri, Debomoy K.; Hicks, Ramona  
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Louisville School of Medicine, Louisville, KY, 40202, USA  
gjkotw01@gwise.louisville.edu  
SOURCE: Diederich, Marc [Editor, Reprint Author]. (2002) pp. 317-322. Cell signaling, transcription, and translation as therapeutic targets. print.  
Publisher: New York Academy of Sciences, 2 East 63rd Street, New York, NY, 10021, USA. Series: Annals of the New York Academy of Sciences.  
Meeting Info.: Conference on Cell Signaling, Transcription and Translation as Therapeutic Targets. Luxembourg, Luxembourg. January 30-February 02, 2002. University Center Luxembourg, Department of Sciences; Doctoral School Medecine et Sante; University Henri Poincare Nancy I; National Research Fund.  
ISSN: 0077-8923 (ISSN print). ISBN: 1-57331-428-5 (cloth), 1-57331-429-3 (paper).  
DOCUMENT TYPE: Book; (Book Chapter)  
Conference; (Meeting)  
Conference; (Meeting Paper)  
LANGUAGE: English  
ENTRY DATE: Entered STN: 19 Mar 2003  
Last Updated on STN: 19 Mar 2003  
TI Potential intervention by **vaccinia virus complement control protein** of the signals contributing to the progression of central nervous system injury to **Alzheimer's** disease.

L4 ANSWER 4 OF 6 MEDLINE on STN DUPLICATE 3  
ACCESSION NUMBER: 2002729264 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 12485887  
TITLE: Potential intervention by **vaccinia virus complement control protein** of the signals contributing to the progression of central nervous system injury to **Alzheimer's** disease.  
AUTHOR: Kotwal Girish J; Lahiri Debomoy K; Hicks Ramona  
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Louisville School of Medicine, Louisville, Kentucky 40202, USA.. gjk01@gwise.louisville.edu  
SOURCE: Annals of the New York Academy of Sciences, (2002 Nov) 973

317-22. Ref: 40  
Journal code: 7506858. ISSN: 0077-8923.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200302  
ENTRY DATE: Entered STN: 20021221  
Last Updated on STN: 20030214  
Entered Medline: 20030213

- TI Potential intervention by **vaccinia virus complement control protein** of the signals contributing to the progression of central nervous system injury to **Alzheimer's** disease.
- AB Traumatic brain injury (TBI) is one of the few known risk factors for **Alzheimer's** disease (AD) and for depression. The mechanisms by which trauma causes delayed cognitive deficits are largely unknown. In recent studies, . . . and other previous studies, it was hypothesized that regulation of the complement system will attenuate the long-term consequences of TBI. **Vaccinia virus complement control protein** (VCP) is a **protein** encoded by **vaccinia** virus. It blocks both the classic and alternative pathways of complement activation in vitro, and by doing so prevents the.

L4 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:212578 CAPLUS  
DOCUMENT NUMBER: 131:57660  
TITLE: Pro-inflammatory **complement** activation by the A $\beta$  peptide of **Alzheimer's** disease is biologically significant and can be blocked by **vaccinia virus complement control protein**  
AUTHOR(S): Daly, James; Kotwal, Girish J.  
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Louisville School of Medicine, Louisville, KY, 40292, USA  
SOURCE: Neurobiology of Aging (1999), Volume Date 1998, 19(6), 619-627  
CODEN: NEAGDO; ISSN: 0197-4580  
PUBLISHER: Elsevier Science Inc.  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

- TI Pro-inflammatory **complement** activation by the A $\beta$  peptide of **Alzheimer's** disease is biologically significant and can be blocked by **vaccinia virus complement control protein**
- AB The amyloid plaque is the hallmark of **Alzheimer's** disease (AD). The transmembrane domain and a portion of the C-terminus (A $\beta$ ) of the amyloid precursor protein, are known to form the nucleus of the amyloid plaque. It has been demonstrated recently, using in vitro assays, that the A $\beta$  peptide can activate both the classical (antibody-independent) and alternate pathways of complement activation. The proposed complement activation is due to the binding of A $\beta$  to the complement components C1q and C3, resp., which initiate formation of the proinflammatory C5a and C5b-9 membrane attack complex. In this report, the authors have investigated the in vitro findings for the likely complement-dependent proinflammatory properties of the **Alzheimer's** disease A $\beta$  peptide. The authors have performed expts. using congenic C5-deficient and C5-sufficient mice injected with synthetic A $\beta$  and recombinant

polypeptide (C-100) containing A $\beta$ . Injection of C-100 into C5-sufficient mice induced a clear increase in the number of polymorphonuclear cells (neutrophils) at the site of injection due to complement activation and the subsequent release of proinflammatory chemotactic factors. In sharp contrast, the C5-deficient mice did not show any increase in cellular influx. The **vaccinia virus complement control**

**protein**, an inhibitor of both the classical and alternate pathway can down-regulate the biol. significant activation of **complement** by A $\beta$ , as demonstrated by an in vitro immunoassay. The therapeutic down-regulation of A $\beta$ -caused complement activation could greatly alleviate the progression of some of the chronic neurodegeneration characteristic of **Alzheimer's** disease.

IT **Proteins**, specific or class

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(VCP (**vaccinia virus complement control protein**); pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Complement**

(activation; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Complement**

RL: ADV (Adverse effect, including toxicity); BIOL (Biological study) (alternative pathway; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Protein sequences**

cdna sequences

(amyloid precursor **protein** C-terminal fragment; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Alzheimer's** disease

Inflammation

**Vaccinia** virus

(pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Amyloid precursor proteins**

RL: ADV (Adverse effect, including toxicity); PRP (Properties); BIOL (Biological study)

(pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Brain**, disease

(senile plaque; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT **Amyloid**

RL: ADV (Adverse effect, including toxicity); BIOL (Biological study) ( $\beta$ -; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia virus complement control protein**)

IT 134548-35-9, 652-751-Glycoprotein (human clone  $\lambda$ APCP168i4 amyloid A4 precursor **protein** moiety reduced)  
 RL: PRP (Properties)  
 (amino acid sequence; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia** virus **complement control protein**)

IT 228092-51-1  
 RL: PRP (Properties)  
 (nucleotide sequence; pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia** virus **complement control protein**)

IT 80295-53-0, **Complement C5**  
 RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)  
 (pro-inflammatory **complement** activation by A $\beta$  peptide of **Alzheimer's** disease is biol. significant and can be blocked by **vaccinia** virus **complement control protein**)

L4 ANSWER 6 OF 6 MEDLINE on STN DUPLICATE 4  
 ACCESSION NUMBER: 1999206442 MEDLINE  
 DOCUMENT NUMBER: PubMed ID: 10192224  
 TITLE: Pro-inflammatory **complement** activation by the A beta peptide of **Alzheimer's** disease is biologically significant and can be blocked by **vaccinia** virus **complement control protein**.  
 AUTHOR: Daly J 4th; Kotwal G J  
 CORPORATE SOURCE: Department of Microbiology and Immunology, University of Louisville School of Medicine, KY 40292, USA.  
 SOURCE: Neurobiology of aging, (1998 Nov-Dec) 19 (6) 619-27.  
 Journal code: 8100437. ISSN: 0197-4580.  
 PUB. COUNTRY: United States  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 199905  
 ENTRY DATE: Entered STN: 19990525  
 Last Updated on STN: 19990525  
 Entered Medline: 19990511

TI Pro-inflammatory **complement** activation by the A beta peptide of **Alzheimer's** disease is biologically significant and can be blocked by **vaccinia** virus **complement control protein**.

AB The amyloid plaque is the hallmark of **Alzheimer's** disease (AD). The transmembrane domain and a portion of the C-terminus (A beta) of the amyloid precursor protein, are known. . . attack complex. In this report, we have investigated the in vitro findings for the likely complement-dependent proinflammatory properties of the **Alzheimer's** disease A beta peptide. We have performed experiments using congenic C5-deficient and C5-sufficient mice injected with synthetic A beta and. . . release of proinflammatory chemotactic factors. In sharp contrast, the C5-deficient mice did not show any increase in cellular influx. The **vaccinia** virus **complement control protein**, an inhibitor of both the classical and alternate pathway can down-regulate the biologically significant activation of **complement** by A beta, as demonstrated by an in vitro immunassay. The therapeutic down-regulation of A beta-caused complement activation could greatly alleviate the progression of some of the chronic neurodegeneration characteristic of **Alzheimer's** disease.

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## 09889624 Results

SEQ ID NO: 1

## SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1453	99.1		263	2	AAY29859	Aay29859 Vaccinia
2	1453	99.1		263	3	AAB13014	Aab13014 Complemen
3	1438	98.1		263	1	AAP92003	Aap92003 Deduced s
4	1405	95.8		263	4	AAB48846	Aab48846 Cowpox vi
5	1396	95.2		263	2	AAY29860	Aay29860 Mutated V
6	1391	94.9		263	2	AAY29858	Aay29858 Vaccinia
7	706	48.2		126	6	ABR57114	Abr57114 MLHR comp
8	472.5	32.2		343	4	AAU87269	Aau87269 Novel cen
9	467	31.9		581	2	AAR13490	Aar13490 Human C4
10	466.5	31.8		645	3	AAB53125	Aab53125 Macaca mu
11	457.5	31.2		363	2	AAW12414	Aaw12414 Porcine c
12	457.5	31.2		363	2	AAY30918	Aay30918 MCP prote
13	438	29.9		302	2	AAR55793	Aar55793 Herpesvir
14	438	29.9		302	2	AAW26320	Aaw26320 Herpesvir
15	438	29.9		360	2	AAR55792	Aar55792 Herpesvir
16	438	29.9		360	2	AAW26319	Aaw26319 Herpesvir
17	432	29.5		559	7	ADE57367	Ade57367 Rat Prote

## RESULT 3

AAP92003

ID AAP92003 standard; protein; 263 AA.

XX

AC AAP92003;

XX

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 17-DEC-2001 (revised)

DT 09-FEB-1990 (first entry)

XX

DE Deduced sequence of complement 4b (C4b) binding protein.

XX

KW Vaccinia virus WR strain; anti-complement protein;

KW complement inactivators; complement 4b; C4b.

XX

OS Vaccinia virus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /label= Signal\_peptide

FT Duplication 20

FT /note= "See note a in comments below."

FT Duplication 83

FT /note= "See note a in comments below."

FT Duplication 144

FT /note= "See note a in comments below."

FT Duplication 202

FT /note= "See note a in comments below."

XX

PN USN7239208-N.

XX

PD 14-MAR-1989.

XX

PF 20-AUG-1988; 88US-00239208.

XX

PR 20-AUG-1988; 88US-00239208.

XX

PA (USSH ) NAT INST OF HEALTH.

PA (USDC ) US SEC OF COMMERCE.

XX



## RESULT 1

US-09-653-813-2

; Sequence 2, Application US/09653813  
; Patent No. 6551595  
; GENERAL INFORMATION:  
; APPLICANT: ROSENGARD, Ariella M.  
; APPLICANT: AHEARN, Joseph M.  
; TITLE OF INVENTION: SMALLPOX INHIBITOR OF COMPLEMENT ENZYMES (SPICE)  
; TITLE OF INVENTION: PROTEIN AND METHODS OF INHIBITING COMPLEMENT ACTIVATION  
; FILE REFERENCE: 9596-107U1  
; CURRENT APPLICATION NUMBER: US/09/653,813  
; CURRENT FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: US 60/076,821  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: WO PCT/US99/04635  
; PRIOR FILING DATE: 1999-03-02  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Vaccinia virus  
US-09-653-813-2

Query Match 99.1%; Score 1453; DB 4; Length 263;  
Best Local Similarity 99.2%; Pred. No. 2.2e-125;  
Matches 261; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKEVSVTFLTLGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCPLPGYRK 60  
|||  
Db 1 MKVESVTFLTLGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCPLPGYRK 60  
  
QY 61 QKMGPIYAKCTGTGWTLFNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120  
|||  
Db 61 QKMGPIYAKCTGTGWTLFNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120  
  
QY 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVITYSCNSGY 180  
|||  
Db 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVITYSCNSGY 180  
  
QY 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
|||  
Db 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
  
QY 241 SGSSSSTCSPGNTWKPELPKCVR 263  
|||  
Db 241 SGSSSSTCSPGNTWKPELPKCVR 263

## RESULT 2

US-07-906-983-2

; Sequence 2, Application US/07906983  
; Patent No. 5187268  
; GENERAL INFORMATION:  
; APPLICANT: Kotwal, Girish  
; APPLICANT: Moss, Bernard  
; TITLE OF INVENTION: Synthetic, Anti-Complement Protein and  
; TITLE OF INVENTION: the Gene Encoding Same  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/906,983
;      FILING DATE:  19920701
;      CLASSIFICATION:  530
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Kenneth A.
;      REGISTRATION NUMBER:  31,677
;      REFERENCE/DOCKET NUMBER:  15280-9
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;      INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-07-906-983-2

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Query Match          98.9%;  Score 1450;  DB 1;  Length 263;
Best Local Similarity 98.9%;  Pred. No. 4.2e-125;
Matches 260;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      1  MKEVSVTFLTLGLIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCPLGYRK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MKVESVTFLTLGLIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCPLGYRK 60

Qy     61  QKMGPIYAKCTGTGWTLFNQCIKRRCPSPRIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  QKMGPIYAKCTGTGWTLFNQCIKRRCPSPRIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120

Qy    121  ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGY 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGY 180

Qy    181  SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKV 240

Qy    241  SGSSSSTCSPGNTWKPELPCVR 263
      ||||||||||||||||||
Db    241  SGSSSSTCSPGNTWKPELPCVR 263

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Result No.	Score	Query Match	Length	DB	ID	Description
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2	407	27.8	608	15	US-10-161-493-112	Sequence 112, App
3	407	27.8	2044	12	US-10-276-774-2152	Sequence 2152, Ap
4	407	27.8	2489	9	US-09-911-842-5	Sequence 5, Appli
5	407	27.8	2489	13	US-10-150-821-5	Sequence 5, Appli
6	391.5	26.7	1033	11	US-09-834-309-1	Sequence 1, Appli
7	391	26.7	279	15	US-10-298-796-25	Sequence 25, Appl
8	391	26.7	421	9	US-09-925-302-732	Sequence 732, App
9	391	26.7	421	14	US-10-106-698-6302	Sequence 6302, Ap
10	372	25.4	66	12	US-10-108-311-1	Sequence 1, Appli
11	372	25.4	66	12	US-10-108-311-2	Sequence 2, Appli
12	350	23.9	254	12	US-10-332-047-10	Sequence 10, Appl
13	350	23.9	271	12	US-10-332-047-11	Sequence 11, Appl
14	350	23.9	314	10	US-09-928-267-27	Sequence 27, Appl
15	350	23.9	314	14	US-10-225-519-11	Sequence 11, Appl

# SUMMARIES

```

      %
Result      Query

```

No.	Score	Match	Length	DB	ID	Description
1	1453	99.1	263	1	WMVZSP	apolipoprotein H h
2	1391	94.9	263	2	T28450	hypothetical prote
3	1385	94.5	263	1	C36838	complement control
4	1385	94.5	263	2	B72152	B18L protein - var
5	493.5	33.7	610	1	I46001	C4b-binding protei
6	486.5	33.2	676	2	A45900	complement C3b rec
7	479	32.7	597	1	S53711	C4BP alpha chain p
8	467	31.9	597	1	NBHUC4	C4b-binding protei
9	465	31.7	558	2	S57953	C4BP protein alpha
10	438	29.9	302	1	WMBE1E	secretory compleme
11	438	29.9	360	1	WMBE2E	membrane-bound com
12	434	29.6	360	2	T42921	complement control
13	432	29.5	497	2	JC2054	complement regulat
14	431.5	29.4	579	2	A56740	sperm-egg recognit
15	428.5	29.2	440	2	A43519	complement recepto

# RESULT 1

## WMVZSP

apolipoprotein H homolog precursor - vaccinia virus

N;Alternate names: 35K secretory protein; C3L protein; virokin

C;Species: vaccinia virus

A;Note: host Homo sapiens (man)

C;Date: 31-Dec-1989 #sequence\_revision 30-Jun-1990 #text\_change 27-Oct-2003

C;Accession: A31005; B42504

R;Kotwal, G.J.; Moss, B.

Nature 335, 176-178, 1988

A;Title: Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.

A;Reference number: A31005; MUID:88318974; PMID:3412473

A;Accession: A31005

A;Molecule type: DNA

A;Residues: 1-263 <KOT>

A;Cross-references: GB:X13166; NID:g60690; PIDN:CAA31564.1; PID:g60691

A;Experimental source: strain WR

R;Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E. Virology 179, 517-563, 1990

A;Title: Appendix to "The complete DNA sequence of vaccinia virus".

A;Reference number: A42501

A;Accession: B42504

A;Molecule type: DNA

A;Residues: 1-263 <GOE>

A;Cross-references: GB:M35027; NID:g335317; PIDN:AAA47997.1; PID:g335345

A;Experimental source: strain Copenhagen

R;Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E. Virology 179, 247-266, 1990

A;Title: The complete DNA sequence of vaccinia virus.

A;Reference number: A42531; MUID:91021027; PMID:2219722

A;Contents: annotation; possible protein-coding frames

A;Note: neither amino acid nor nucleotide sequence is given

C;Superfamily: complement control protein; complement factor H repeat homology

C;Keywords: duplication; extracellular protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-263/Product: C4b-binding protein homolog #status predicted <MAT>

F;21-81/Domain: complement factor H repeat homology <FH1>

F;86-143/Domain: complement factor H repeat homology <FH2>

F;148-201/Domain: complement factor H repeat homology <FH3>

F;206-261/Domain: complement factor H repeat homology <FH4>

Query Match 99.1%; Score 1453; DB 1; Length 263;

Best Local Similarity 99.2%; Pred. No. 9.1e-96;

Matches 261; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MKEVSVTFLTLGLGICVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRK 60
          || |||||
Db      1 MKVESVTFLTLGLGICVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRK 60

Qy     61 QKMGPIYAKCTGTGTWTLFNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120
          |||||
Db     61 QKMGPIYAKCTGTGTWTLFNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120

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Qy 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVITYSCNSGY 180  
 |||||  
 Db 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVITYSCNSGY 180  
 |||||  
 Qy 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
 |||||  
 Db 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
 |||||  
 Qy 241 SGSSSSSTCSPGNTWKPELPCVR 263  
 |||||  
 Db 241 SGSSSSSTCSPGNTWKPELPCVR 263

# RESULT 2

T28450

hypothetical protein D15L - variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 27-Oct-2003

C;Accession: T28450

R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin, L.; Yuran, T.E.; Parsons, J.M.; Loparev, V.N.

Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus genome.

A;Reference number: Z20488; MUID:94088747; PMID:8264798

A;Accession: T28450

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-263 <MAS>

A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60760.1; PID:g438930

A;Experimental source: strain "Bangladesh-1975"

C;Superfamily: complement control protein; complement factor H repeat homology

Query Match 94.9%; Score 1391; DB 2; Length 263;  
 Best Local Similarity 94.7%; Pred. No. 2.2e-91;  
 Matches 249; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MKEVSVTFLTLGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCCLPGYRK 60  
 |||||  
 Db 1 MKVERVTFLTLGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCCLPGYRK 60  
 |||||  
 Qy 61 QKMGPIYAKCTGTGWTFLNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120  
 |||||  
 Db 61 QKMGPIYAKCTGTGWTFLNQCIKRRCPSPRDIDNGHLDIGGVDFGSSITYSCNSGYLLIG 120  
 |||||  
 Qy 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVITYSCNSGY 180  
 |||||  
 Db 121 EYKSYCKLGSTGSMVWNPKAPICESVKCQLPPSISNGRHNGYNDFYTDGSVVITYSCNSGY 180  
 |||||  
 Qy 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
 |||||  
 Db 181 SLIGNSGVLCSGGEWSNPPTCQIVKCPHPTILNGYLSSGFKRSYSYNDNVDFTKYGYKL 240  
 |||||  
 Qy 241 SGSSSSSTCSPGNTWKPELPCVR 263  
 |||||  
 Db 241 SGSSSSSTCSPGNTWQPELPCVR 263

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1453	99.1	263	1	VCP_VACCV	P10998 vaccinia vi
2	493.5	33.7	610	1	C4BP_BOVIN	Q28065 bos taurus
3	467	31.9	597	1	C4BP_HUMAN	P04003 homo sapien
4	465	31.7	558	1	C4BP_RAT	Q63514 rattus norv
5	438	29.9	360	1	CCPH_HSVSA	Q01016 herpesvirus
6	413	28.2	469	1	C4BP_MOUSE	P08607 mus musculu

7	407	27.8	2039	1	CR1_HUMAN	P17927	homo sapien
8	391.5	26.7	1033	1	CR2_HUMAN	P20023	homo sapien
9	391	26.7	377	1	MCP_HUMAN	P15529	homo sapien
10	382.5	26.1	390	1	DAF1_MOUSE	Q61475	mus musculu
11	382	26.1	379	1	MCP_CAVPO	P70105	cavia porce
12	350	23.9	381	1	DAF_HUMAN	P08174	homo sapien
13	347.5	23.7	1025	1	CR2_MOUSE	P19070	mus musculu
14	347	23.7	340	1	DAF_PONPY	P49457	pongo pygma
15	340.5	23.2	407	1	DAF2_MOUSE	Q61476	mus musculu
16	333.5	22.7	3565	1	CSM1_HUMAN	Q96pz7	homo sapien
17	331.5	22.6	668	1	F13B_MOUSE	Q07968	mus musculu
18	317	21.6	317	1	VB05_VACCL	P24083	vaccinia vi
19	317	21.6	661	1	F13B_HUMAN	P05160	homo sapien
20	314.5	21.5	2796	1	CSM3_MOUSE	Q80t79	mus musculu

# RESULT 1

## VCP\_VACCV

ID VCP\_VACCV STANDARD; PRT; 263 AA.

AC P10998;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Complement control protein precursor (VCP) (Secretory protein 35)

DE (Protein C3) (28 kDa protein).

GN C3L.

OS Vaccinia virus (strain WR), and

OS Vaccinia virus (strain Copenhagen).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI\_TaxID=10254, 10249;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.

RC STRAIN=WR;

RX MEDLINE=88318974; PubMed=3412473;

RA Kotwal G.J., Moss B.;

RT "Vaccinia virus encodes a secretory polypeptide structurally related

RT to complement control proteins.";

RL Nature 335:176-178(1988).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=WR;

RX MEDLINE=89073756; PubMed=2849238;

RA Kotwal G.J., Moss B.;

RT "Analysis of a large cluster of nonessential genes deleted from a

RT vaccinia virus terminal transposition mutant.";

RL Virology 167:524-537(1988).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Copenhagen;

RX MEDLINE=91021027; PubMed=2219722;

RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,

RA Paoletti E.;

RT "The complete DNA sequence of vaccinia virus.";

RL Virology 179:247-266(1990).

RN [4]

RP COMPLETE GENOME.

RC STRAIN=Copenhagen;

RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,

RA Paoletti E.;

RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";

RL Virology 179:517-563(1990).

RN [5]

RP FUNCTION.

RX MEDLINE=92115714; PubMed=1731333;

RA Isaacs S.N., Kotwal G.J., Moss B.;

RT "Vaccinia virus complement-control protein prevents

RT antibody-dependent complement-enhanced neutralization of infectivity

RT and contributes to virulence.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).

RN [6]

RP STRUCTURE BY NMR OF 146-263.  
 RX MEDLINE=97446168; PubMed=9299352;  
 RA Wiles A.P., Shaw G., Bright J., Perczel A., Campbell I.D.,  
 RA Barlow P.N.;  
 RT "NMR studies of a viral protein that mimics the regulators of  
 RT complement activation.";  
 RL J. Mol. Biol. 272:253-265(1997).  
 CC -!- FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY  
 CC INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT  
 CC ACTIVATION. BINDS C3B AND C4B.  
 CC -!- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF  
 CC COMPLEMENT ACTIVATION (RCA).  
 CC -!- SIMILARITY: Contains 4 Sushi (SCR) domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X13166; CAA31564.1; -.  
 DR EMBL; M22812; AAA69605.1; -.  
 DR EMBL; M35027; AAA47997.1; -.  
 DR PIR; A31005; WMVZSP.  
 DR PDB; 1VVC; 03-DEC-97.  
 DR PDB; 1VVD; 03-DEC-97.  
 DR PDB; 1VVE; 03-DEC-97.  
 DR PDB; 1E5G; 26-APR-01.  
 DR PDB; 1G40; 07-FEB-01.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00084; sushi; 4.  
 DR SMART; SM00032; CCP; 4.  
 KW Signal; Repeat; Sushi; 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 263 COMPLEMENT CONTROL PROTEIN.  
 FT DOMAIN 20 82 SUSHI 1.  
 FT DOMAIN 85 144 SUSHI 2.  
 FT DOMAIN 147 202 SUSHI 3.  
 FT DOMAIN 205 262 SUSHI 4.  
 FT DISULFID 21 70 BY SIMILARITY.  
 FT DISULFID 54 81 BY SIMILARITY.  
 FT DISULFID 86 126 BY SIMILARITY.  
 FT DISULFID 112 143 BY SIMILARITY.  
 FT DISULFID 148 190 BY SIMILARITY.  
 FT DISULFID 176 201 BY SIMILARITY.  
 FT DISULFID 206 248 BY SIMILARITY.  
 FT DISULFID 234 261 BY SIMILARITY.  
 FT STRAND 154 154  
 FT TURN 155 156  
 FT STRAND 157 159  
 FT STRAND 170 170  
 FT STRAND 174 176  
 FT TURN 178 179  
 FT STRAND 181 183  
 FT STRAND 189 190  
 FT STRAND 195 196  
 FT STRAND 200 202  
 FT STRAND 216 216  
 FT STRAND 227 232  
 FT STRAND 239 240  
 FT STRAND 245 249  
 FT TURN 250 252  
 FT STRAND 253 255  
 FT STRAND 261 263  
 SQ SEQUENCE 263 AA; 28629 MW; E4322CC9A6EF8997 CRC64;

Query Match 99.1%; Score 1453; DB 1; Length 263;  
 Best Local Similarity 99.2%; Pred. No. 6e-107;  
 Matches 261; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Qy 1 MKEVSVTFLTLGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRK 60  
 |||  
 Db 1 MKVESVTFLTLGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRK 60

Qy 61 QKMGPIYAKCTGTGWTFLNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120  
 |||  
 Db 61 QKMGPIYAKCTGTGWTFLNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120

Qy 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNHGYEDFYTDGSSVVTYSCNSGY 180  
 |||  
 Db 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNHGYEDFYTDGSSVVTYSCNSGY 180

Qy 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
 |||  
 Db 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240

Qy 241 SGSSSSTCSPGNTWKPELPCVR 263  
 |||  
 Db 241 SGSSSSTCSPGNTWKPELPCVR 263

Result No.	Score	Query Match	Length	DB	ID	Description
1	1443	98.4	263	12	Q7TDW7	Q7tdw7 ectromelia
2	1402	95.6	265	12	Q8V2Z4	Q8v2z4 camelpox vi
3	1391	94.9	263	12	Q89859	Q89859 variola vir
4	1385	94.5	263	12	Q89061	Q89061 variola vir
5	1385	94.5	263	12	Q8QN28	Q8qn28 cowpox viru
6	1385	94.5	263	12	Q89076	Q89076 variola vir
7	1385	94.5	263	12	Q07033	Q07033 variola vir
8	1384	94.4	259	12	P87616	P87616 cowpox viru
9	1350	92.1	262	12	Q8JLI5	Q8jli5 ectromelia
10	1345	91.7	262	12	Q7TDW6	Q7tdw6 ectromelia
11	1339	91.3	260	12	Q7TDW5	Q7tdw5 ectromelia
12	1118.5	76.3	216	12	Q98VL5	Q98v15 monkeypox v
13	491.5	33.5	365	6	Q7YRJ3	Q7yrj3 bos taurus
14	486.5	33.2	679	11	Q99254	Q99254 mus musculu
15	466.5	31.8	645	12	Q9WRU2	Q9wru2 macaca mula
16	466	31.8	533	11	O08569	O08569 cavia porce
17	457.5	31.2	363	6	O02839	O02839 sus scrofa

# RESULT 7

Q07033

ID Q07033 PRELIMINARY; PRT; 263 AA.

AC Q07033;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE D12L protein.

GN D12L.

OS Variola virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI\_TaxID=10255;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=India-1967;

RA Blinov V.M.;

RL Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=India-1967;

RX MEDLINE=93202281; PubMed=8384129;

RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;

RT "Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";

RL FEBS Lett. 319:80-83(1993).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=95159666; PubMed=7856312;  
 RA Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,  
 RA Olenina L.V., Chirikova G.B., Sandakhchiev L.S.;  
 RT "Analysis of the nucleotide sequence of 53 kbp from the right terminus  
 of the genome of variola major virus strain India-1967.";  
 RL Virus Res. 34:207-236(1994).

RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=95320969; PubMed=7597802;  
 RA Shchelkunov S.N., Totmenin A.V.;  
 RT "Two types of deletions in orthopoxvirus genomes.";  
 RL Virus Genes 9:231-245(1995).

RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=96290243; PubMed=8725113;  
 RA Shchelkunov S.N., Totmenin A.V., Sandakhchiev L.S.;  
 RT "Analysis of the nucleotide sequence of 23.8 kbp from the left  
 terminus of the genome of variola major virus strain India-1967.";  
 RL Virus Res. 40:169-183(1996).  
 DR EMBL; X69198; CAA48953.1; -.  
 DR PIR; C36838; C36838.  
 DR HSSP; P10998; 1VVD.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00084; sushi; 4.  
 DR SMART; SM00032; CCP; 4.  
 SQ SEQUENCE 263 AA; 28789 MW; 5FE244F48B19D479 CRC64;

Query Match 94.5%; Score 1385; DB 12; Length 263;  
 Best Local Similarity 94.3%; Pred. No. 1.2e-117;  
 Matches 248; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MKEVSVTFLTLTGIGCVLSCCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCCLPGYRK 60  
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 Db 1 MKVERVTFLTLTGIGCVLSCCTIPSRPINMTFKNSVETDANANYNIGDTIEYLCCLPGYRK 60  
 Qy 61 QKMGPPIYAKCTGTGWTLEFNQCIKRRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIG 120  
 |||||:|||||  
 Db 61 QKMGPPIYAKCTGTGWTLEFNQCIKRRCPSPRDIDNGHLDIGGVDFGSSITYSCNSGYLLIG 120  
 Qy 121 ESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNGRHNGYEDFYTDGSVVITYSCNSGY 180  
 |||||:|||||:|||||  
 Db 121 EYKSYCKLGSTGSMVWNPKAPICESVKCQLPPSISNGRHNGYNDFYTDGSVVITYSCNSGY 180  
 Qy 181 SLIGNSGVLCSGGEWSDPPTCQIVKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKL 240  
 |||||:|||||:|||||  
 Db 181 SLIGNSGVLCSGGEWSNPPTCQIVKCPHPTILNGYLSSGFKRSYSYNDNVDFTKYGYKL 240  
 Qy 241 SGSSSSTCSPGNTWKPELPCVVR 263  
 |||||:|||||  
 Db 241 SGSSSSTCSPGNTWQPELPCVVR 263